

	YY-1		AP-1	
SAA1	--TAGATATG	AACTCAGAGG	GACTTCATTT	CAGAGGCATC TGCCATGTGG ⁻³⁹¹
SAA2	TTTAGACATG	AACTCACAGG	GATTTTCAGT-	CAGGGTCATC TGCCATGTGG ⁻³⁹⁷
	*****	***	*****	***
	AP-2		NEIL-6/YY-1	
SAA1	CCCAGCAGAG	CCCATCCTGA	GGAAATGACT	GGTAGAGTCA GGAGCTGGCT ⁻³⁴¹
SAA2	CCCAGCAGGG	CCCATCCTGA	GGAAATGACC	GGTATAGTCA GGAGCTGGCT ⁻³⁴⁷
	*****	*	*****	*****
				YY-1
SAA1	TCAAAGCTGC	CCTCACTTCA	CACCTTCCAG	CAGCCCAGGT GCCGCCATCA ⁻²⁹¹
SAA2	GAAGAGCTGC	CCTCACTCCA	CACCTTCCAG	CAGCCCAGGT GCCGCCATCA ⁻²⁹⁷
	*	*****	*****	*****
	NFkB		AP-2	SAF
SAA1	CGGGGCTCCC	ACTCTCAACT	CCGCAGCCTC	AGCCCCCTCA ATGCTGAGGA ⁻²⁴¹
SAA2	CGGGGCTCCC	ACTGGCATCT	CTGCAGCTGC	ACTTCCCCCA ATGCTGAGGA ⁻²⁴⁷
	*****	***	***	***
	-240			
SAA1	GCAGAGCTGG	TCTCCTGCCC	TGACAGCTGC	CA-GGCACA- -----TC ⁻²⁰¹
SAA2	GCAGAGCTGA	TCTAGACCCC	TGTCCATTGC	CAAGGCACAG CAAACCTCTC ⁻¹⁹⁷
	*****	***	***	***
	-200	GRE	NE-IL6/STAT	AP-1.....
SAA1	TTGTTCCCTC	AGGTTGCACA	ACTGGGATAA	ATGACCCGGG ATGAAGAAAC ⁻¹⁵¹
SAA2	TTGTTCCCAT	AGGTTACACA	ACTGGGATAA	ATGACCCGGG ATGAAGAAAC ⁻¹⁴⁷
	*****	*****	*****	*****
	-150			YY-1
SAA1	CACTGGCATC	CAGGAAGTTG	TCTTAGACCG	TTTTGTAGGG GAAATGACCT ⁻¹⁰¹
SAA2	CACCGGCATC	CAGGAAGTTG	TCTTAGACCA	GTTTGTAGGG GAAATGACCT ⁻⁹⁷
	***	*****	*****	*****
	-100	NFkB		
SAA1	GCAGGGACTT	TCCCAGGGA	CCACATCCAG	CTTTTCTTCC CTCCAAGAA ⁻⁵¹
SAA2	GCAGGGACTT	TCCCAGGGA	CCACATCCAG	CTTTTCTTCC CTCCAAGAG ⁻⁴⁷
	*****	*****	*****	*****
	-50	SP-1		
SAA1	ACCAGCAGGG	AAGGCTCAGT	ATAAATAGCA	GCCACCGCTC CCTGGCAGGC ⁻¹
SAA2	ACCAGCA---	-AGGCTCACT	ATAAATAGCA	GCCACCTCTC CCTGGCAGAC ⁻¹
	*****	*****	*****	*****

FIG. 1

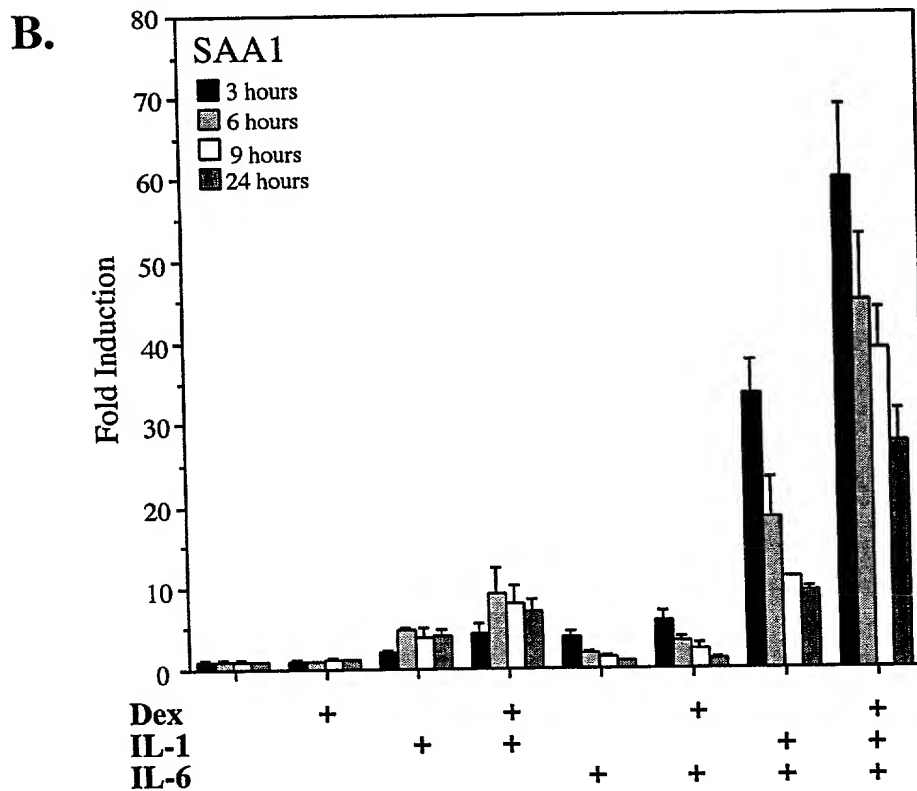
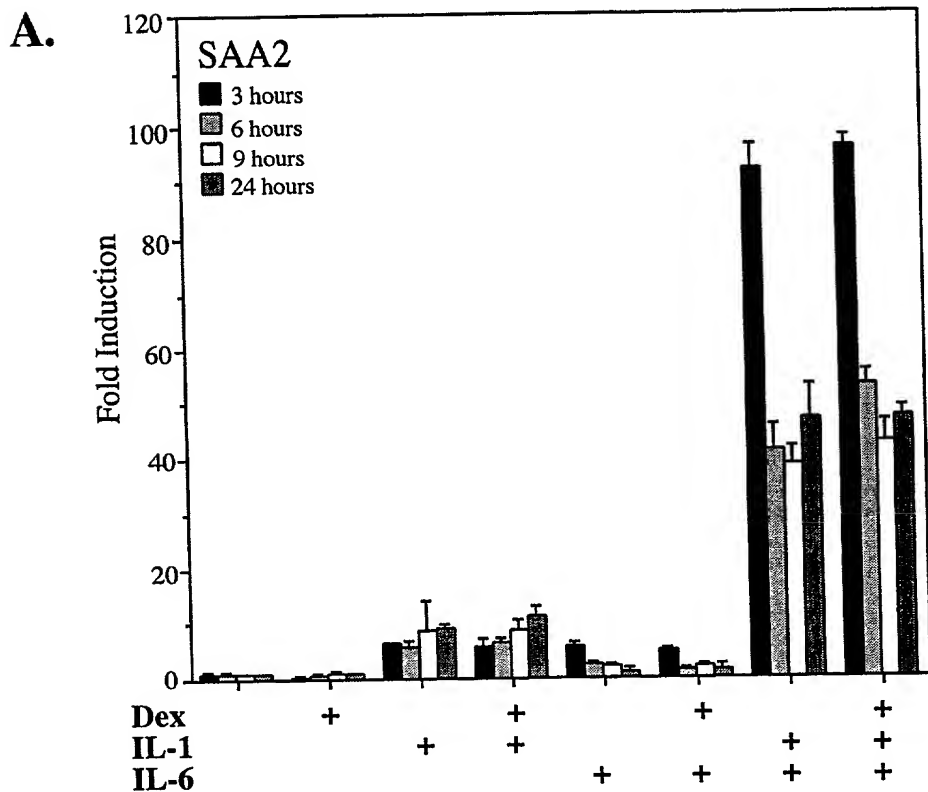


FIG. 2

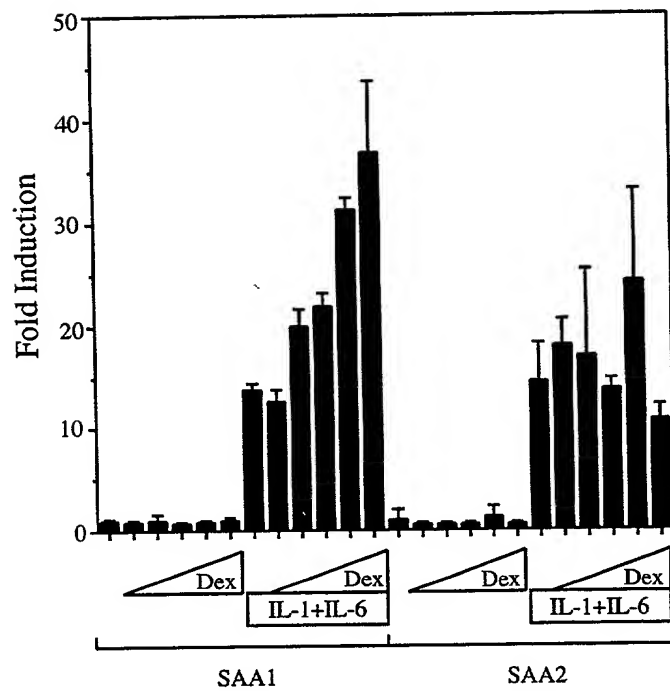


FIG. 3

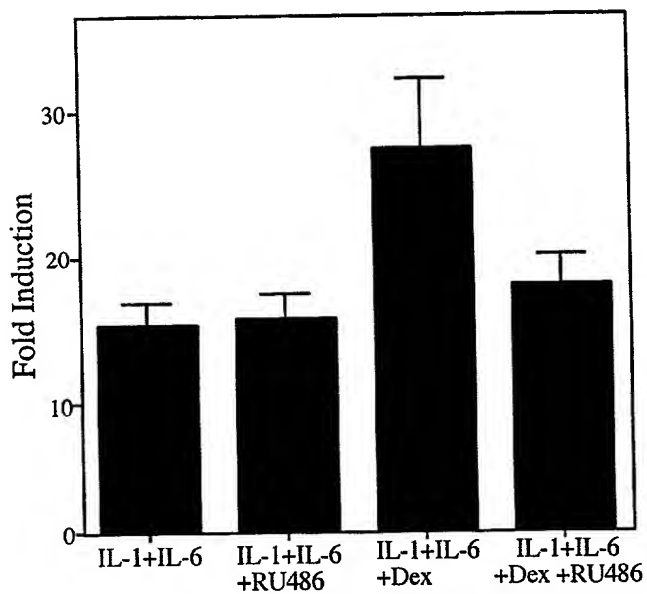


FIG. 4

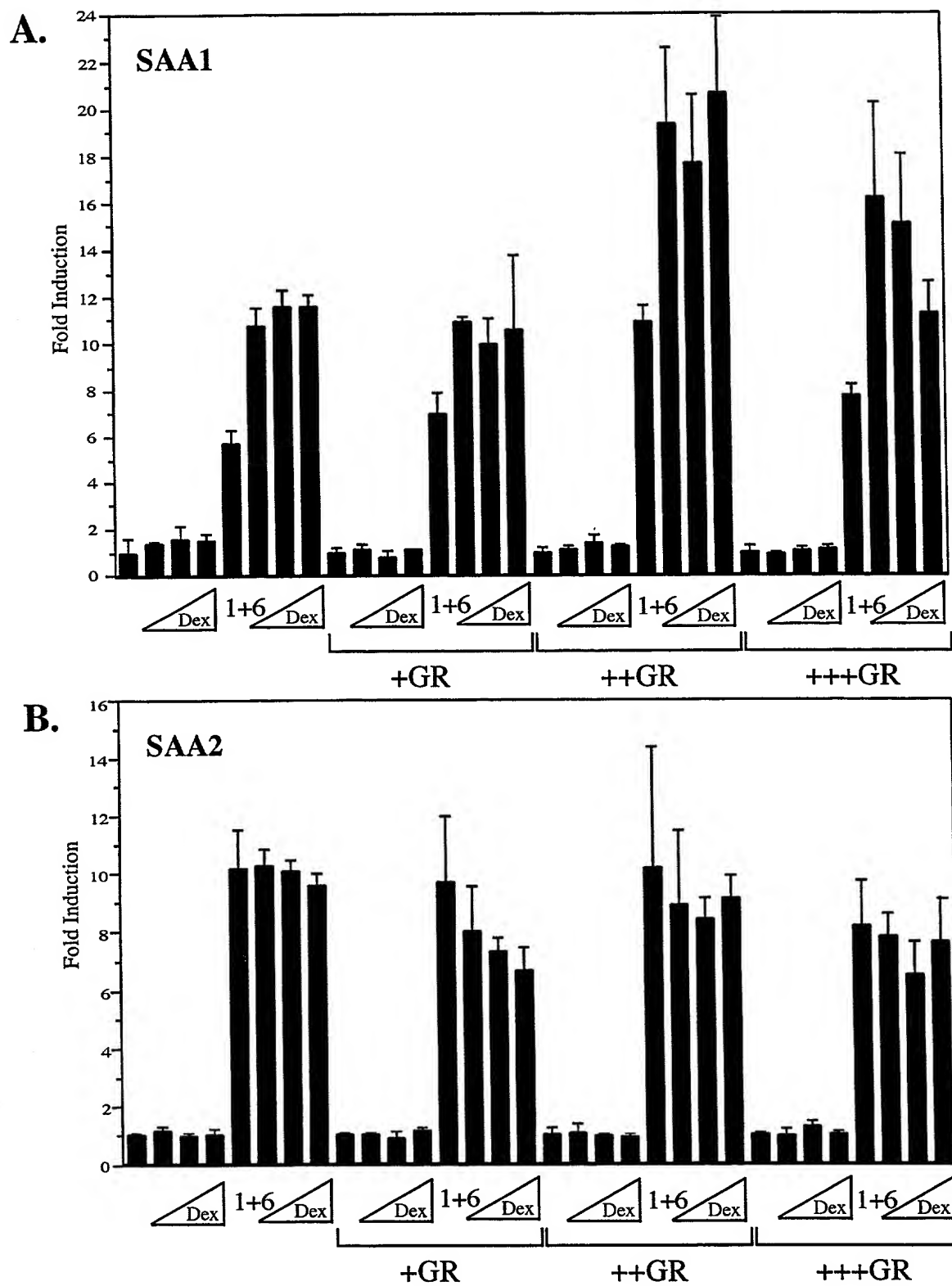


FIG. 5

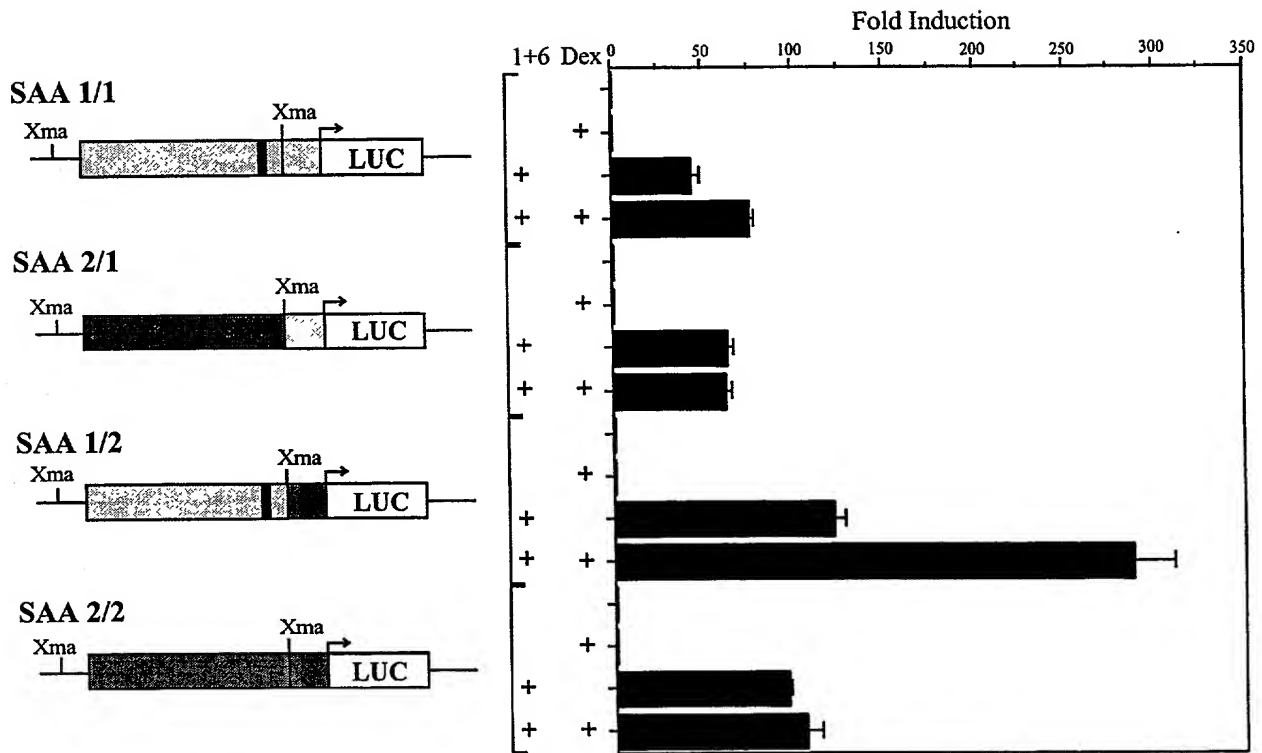


FIG. 6

A.

SAA1	CA- <u>GGCACA</u> -----TCTTGTTCCCTCAGGTTGCACA
GREI	CA-GGCACAGCAAACCTCTCTTGTTCCCTCAGGTTGCACA
GRED	CAAGGCACA-----TCTTGTTCCCATAGGTTACACA
SAA2	CAAGGCACAGCAAACCTCTCTTGTTCCCATAGGTTACACA
Consensus	GGTACA NNNTGTTCT
GRE	

B.

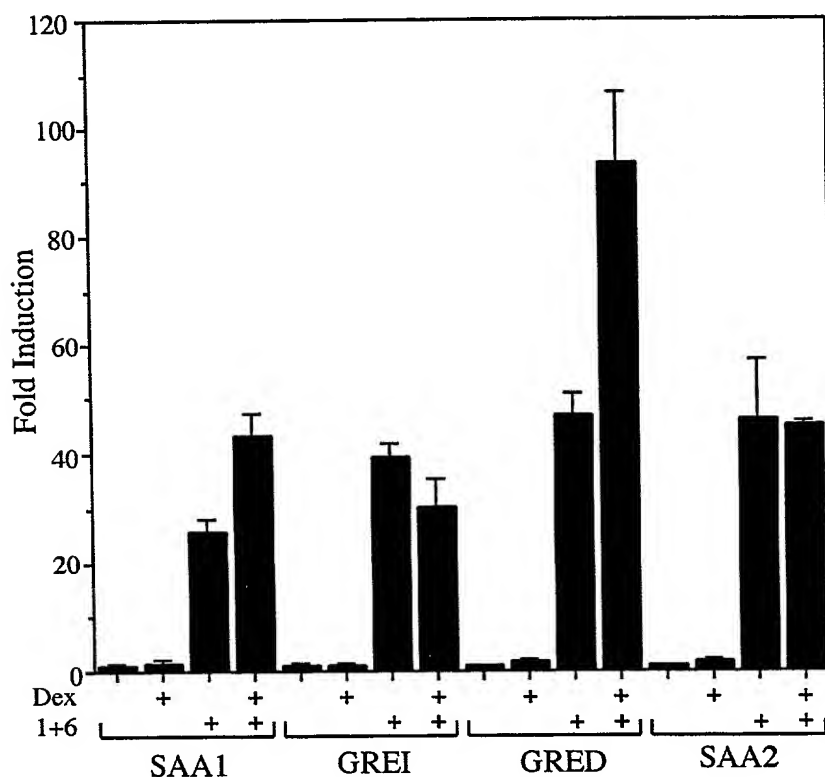


FIG. 7

A.

SAA1 CAGACAAATACTTCCATGCTCGGGGGACTATGATGCTGCCAAAAGGGGACCTGGGGGTG²⁴⁶
SAA2 CAGACAAATACTTCCATGCTCGGGGGACTATGATGCTGCCAAAAGGGGACCTGGGGGTG²⁴⁶

 exon3 exon4

SAA1 TCTGGGCTGCAGAAGCGATCAG|CGATG—//—//—TGAGCTTCCTCTTCACTCTGCTC⁴²⁶
SAA2 CCTGGGCCGCAGAAGTGATCAG|CAATG—//—//—TGAGCTTCCTCTTCACTCTGCTC⁴²⁶

SAA1 TCAGGAGATCTGGCTGTGAGGC-TCAGGGCAGGGATACAAAGC----GGGG-----⁴⁷²
SAA2 TCAGGAGACCTGGCTATGAGCCCTCGGGGCAGGGATTCAAAGTTAGTGAGGTCTATGTCC⁴⁸⁶

SAA1 AGAG-----GGTACACAATGGGTATCTAATAAATACTTAAGAGGTGGAAAAAA⁵²⁰
SAA2 AGAGAAGCTGAGATATGGCATATAATAGGCATCTAATAAATGCTTAAGAGGTGGAAAAAA⁵⁴⁶

B.

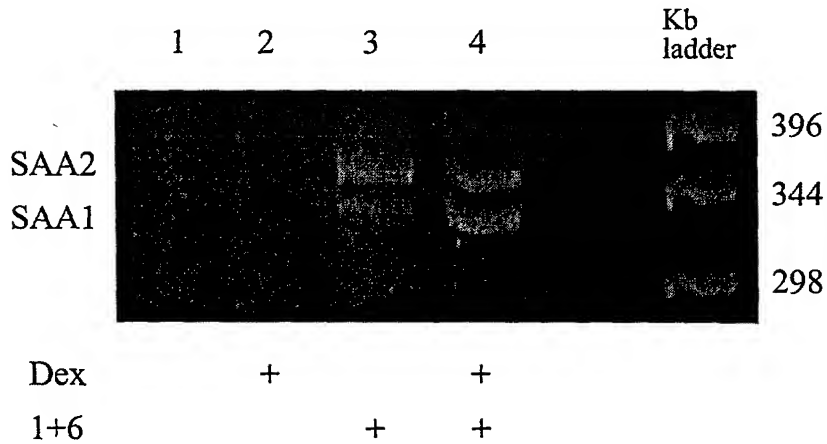


FIG. 8